WHAT IS CLAIMED IS:

1. A method of identifying a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide probe comprising a sequence identical or complementary to at least 10 consecutive nucleotides contained in SEQ ID NO:224, such that the probe hybridizes to the nucleic acid;

b) detecting any hybrid formed as a result of a); and

c) identifying the nucleic acid as encoding at least a portion of human telomerase reverse transcriptase (hTRT) if the hybrid is detected.

2. A method of detecting a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide probe such that the probe hybridizes to a nucleic acid comprising at least 100 consecutive nucleotides contained in SEQ ID NO:224 if present in the sample; and

b) detecting any hybrid formed as a result of a);

wherein the polynucleotide probe comprises a sequence identical or complementary to at least 25 consecutive nucleotides contained in SEQ ID NO:224.

3. The method of claim 2, wherein the nucleic acid is human genomic DNA.

4. The method of claim 2, wherein the nucleic acid is human mRNA.

5. The method of claim 2, wherein the nucleic acid comprises at least 250 nucleotides of SEQ ID NO:224.

6. The method of claim 2, wherein the nucleic acid comprises at least 500 nucleotides of SEQ ID NO:224.

7. The method of claim 2, wherein the probe comprises a sequence identical or complementary to at least 30 consecutive nucleotides contained in SEQ ID NO:224.

8. The method of claim 2, wherein the probe comprises a sequence identical or complementary to at least 50 consecutive nucleotides contained in SEQ ID NO:224.

9. The method of claim 2, wherein the probe comprises a sequence identical or complementary to at least 100 consecutive nucleotides contained in SEQ ID NO:224.

10. The method of claim 2, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.

11. The method of claim 9, wherein the probe comprises a sequence not contained in SEQ. ID NO:62.

12. The method of claim 2, wherein the sample is a human biological sample.

13. A method of identifying a nucleic acid in a sample, comprising:

a) combining the sample with a polynucleotide primer containing a sequence identical or complementary to at least 10 consecutive nucleotides contained in SEQ ID NO:224, under conditions that the primer amplifies the nucleic acid;

b) detecting any amplification product formed as a result of a); and

c) identifying the nucleic acid as encoding at least a portion of hTRT if the amplification product is detected.

14. A method of detecting a nucleic acid encoding at least a portion of human telomerase reverse transcriptase (hTRT) in a sample, comprising:

a) combining the sample with a polynucleotide primer such that the primer amplifies nucleic acid encoding at least a portion of hTRT if present in the sample; and

b) detecting any amplified product formed as a result of a);

wherein the polynucleotide primer comprises a sequence identical or complementary to at least 15 consecutive nucleotides contained in SEQ ID NO:224.

15. The method of claim 14, wherein the polynucleotide primer comprises a sequence identical or complementary to at least 30 consecutive nucleotides contained in SEQ ID NO:224.

16. The method of claim 14, wherein the polynucleotide primer comprises a sequence identical or complementary to at least 50 consecutive nucleotides contained in SEQ ID NO:224.

17. The method of claim 14, wherein the sample is a human biological sample.

18. The method of claim 14, wherein the sample comprises human genomic DNA.

19. The method of claim 14, wherein the sample comprises human mRNA.

20. The method of claim 14, wherein the primer comprises a sequence identical or complementary to at least 100 consecutive nucleotides contained in SEQ ID NO:224.

21. The method of claim 14, wherein the primer comprises a sequence not contained in SEQ. ID NO:62.

22. The method of claim 20, wherein the primer comprises a sequence not contained in SEQ. ID NO:62.

23. A combination of oligonucleotide primers for PCR amplification, comprising a first primer that hybridizes to a polynucleotide consisting of SEQ ID NO:224 under stringent amplification conditions, and a second primer that hybridizes to the complement of said nucleic acid under stringent amplification conditions.

24. The combination of primers of claim 23, wherein either primer comprises between 15-30 nucleotides.

25. The combination of primers of claim 23, wherein either primer comprises between 20-25 nucleotides.

26. The combination of primers of claim 23, wherein 50% or more of the nucleotides of either primer are guanine and/or cytosine.

27. A PCR product that hybridizes under stringent conditions to a polynucleotide having a sequence consisting of SEQ ID NO:224 or its complement.

28. A hybridization complex comprising:

a) one strand of a cellular hTRT nucleic acid; and

b) one strand of nucleic acid comprising a recombinant or synthetic fragment of hTRT;

wherein said fragment of hTRT comprises at least 10 contiguous nucleotides of SEQ ID NO:224 or its complement.

29. The hybridization complex of claim 28, wherein the hTRT nucleic acid is an hTRT mRNA.

30. The hybridization complex of claim 28, wherein the hTRT nucleic acid is an hTRT cDNA.

31. The hybridization complex of claim 28, wherein the fragment comprises at least 20 contiguous nucleotides of SEQ ID NO:224 or its complement.

32. The hybridization complex of claim 28, wherein the fragment comprises 10-100 contiguous nucleotides of SEQ ID NO:224 or its complement.

33. The hybridization complex of claim 28, wherein said hybridization complex is a DNA:DNA complex.

34. The hybridization complex of claim 28, wherein said hybridization complex is a DNA:RNA complex.